

[Please substitute the following claim 2 for the currently pending claim 2:]

2. (Once amended) A nucleic acid polymerase which has been modified to reduce or eliminate misincorporation of nucleotides during nucleic acid synthesis, wherein said modification corresponds to amino acid position Arg722, or Lys726, or Arg722 and Lys726 of a *Thermotoga neopolitana* polymerase.

[Please substitute the following claim 3 for the currently pending claim 3:]

3. (Once amended) The polymerase of claim 1 or 2, wherein said polymerase is a DNA polymerase.

[Please substitute the following claim 4 for the currently pending claim 4:]

4. (Once amended) The polymerase of claim 3, wherein said polymerase is derived from a mesophilic organism or said polymerase is thermostable.

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[Please substitute the following claim 5 for the currently pending claim 5:]

5. (Once amended) The polymerase of claim 3, wherein said polymerase is selected from the group consisting of *Tne* DNA polymerase, *Taq* DNA polymerase, *Tma* DNA polymerase, *Tth* DNA polymerase, *Tli* (VENT™) DNA polymerase, *Pfu* DNA polymerase, DEEPVENT™ DNA polymerase, *Pwo* DNA polymerase, *Bst* DNA polymerase, *Bca* DNA polymerase, *Tfl* DNA polymerase, and mutants and fragments thereof.

[Please substitute the following claim 6 for the currently pending claim 6:]

6. (Once amended) The polymerase of claim 1 or 2, further comprising one

or more modifications to reduce or eliminate one or more activities selected from the group consisting of:

- (a) the 3'→5' exonuclease activity of the polymerase;
- (b) the 5'→3' exonuclease activity of the polymerase; and
- (c) the discriminatory activity against one or more dideoxynucleotides.

[Please substitute the following claim 7 for the currently pending claim 7:]

7. (Once amended) The polymerase of claim 1 or claim 2, wherein said polymerase is modified to reduce or eliminate 3'→5' exonuclease activity.

[Please substitute the following claim 8 for the currently pending claim 8:]

8. (Once amended) The polymerase of claim 1 or claim 2, wherein said polymerase is modified to reduce or eliminate discriminatory activity against one or more dideoxynucleotides.

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[Please substitute the following claim 9 for the currently pending claim 9:]

9. (Once amended) The polymerase of claim 1 or claim 2, wherein said polymerase is modified to reduce or eliminate 5'→3' exonuclease activity.

Please substitute the following claim 11 for the currently pending claim 11:

11. (Once amended) The polymerase of claim 1, wherein said modification is in an O-helix of said polymerase.

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[Please substitute the following claim 12 for the currently pending claim 12:]

12. (Once amended) The polymerase of claim 1 or claim 2, wherein said modification corresponds to amino acid position R (Arg722).

Please substitute the following claim 14 for the currently pending claim 14:

14. (Once amended) The polymerase of claim 12, wherein R (Arg722) is substituted with an amino acid selected from the group consisting of Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

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[Please substitute the following claim 15 for the currently pending claim 15:]

15. (Once amended) The polymerase of claim 1 or claim 2, wherein said modification corresponds to amino acid position K (Lys726).

Please substitute the following claim 17 for the currently pending claim 17:

17. (Once amended) The polymerase of claim 15, wherein K (Lys726) is substituted with an amino acid selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

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[Please substitute the following claim 18 for the currently pending claim 18:]

18. (Once amended) The polymerase of claim 1 or claim 2, wherein said modifications correspond to amino acid at position R (Arg722) and at position K (Lys726).

Please substitute the following claim 20 for the currently pending claim 20:

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20. (Once amended) The polymerase of claim 18, wherein R (Arg722) is substituted with an amino acid selected from the group consisting of Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val, and wherein K (Lys726) is substituted with an amino acid selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

Please add the following claims:

43. (New) The polymerase of claim 1 or 2, wherein said polymerase is a RNA polymerase.

44. (New) The polymerase of claim 43, wherein said RNA polymerase is selected from the group consisting of T3, T5 and SP6.

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45. (New) The polymerase of claim 1 or 2, wherein said polymerase has substantially reduced or lacks 3'-5' exonuclease activity.

46. (New) The polymerase of claim 1 or 2, wherein said polymerase has substantially reduced or lacks 5'-3' exonuclease activity.

47. (New) A nucleic acid polymerase which has been modified, wherein said modification corresponds to amino acid position Arg722, or Lys726, or Arg722 and Lys726 of a *Thermotoga neopolitana* polymerase.

48. (New) The polymerase of claim 47, wherein said polymerase is a DNA polymerase.

49. (New) The polymerase of claim 48, wherein said polymerase is derived from a mesophilic organism or said polymerase is thermostable.

50. (New) The polymerase of claim 48, wherein said polymerase is selected from the group consisting of *Tne* DNA polymerase, *Taq* DNA polymerase, *Tma* DNA polymerase, *Tth* DNA polymerase, *Tli* (VENT™) DNA polymerase, *Pfu* DNA polymerase, DEEPVENT™ DNA polymerase, *Pwo* DNA polymerase, *Bst* DNA polymerase, *Bca* DNA polymerase, *Tfl* DNA polymerase, and mutants and fragments thereof.

51. (New) The polymerase of claim 47, further comprising one or more modifications to reduce or eliminate one or more activities selected from the group consisting of:

- (a) the 3'→5' exonuclease activity of the polymerase;
- (b) the 5'→3' exonuclease activity of the polymerase; and
- (c) the discriminatory activity against one or more

dideoxynucleotides.

52. (New) The polymerase of claim 47, wherein said polymerase is modified to reduce or eliminate 3'→5' exonuclease activity.

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53. (New) The polymerase of claim 47, wherein said polymerase is modified to reduce or eliminate discriminatory activity against one or more dideoxynucleotides.

54. (New) The polymerase of claim 47, wherein said polymerase is modified to reduce or eliminate 5'→3' exonuclease activity.

55. (New) The polymerase of claim 47, wherein said modification is in an O-helix of said polymerase.

56. (New) The polymerase of claim 47, wherein said modification corresponds to amino acid position R (Arg722).

57. (New) The polymerase of claim 56, wherein R (Arg722) is substituted with an amino acid selected from the group consisting of Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

58. (New) The polymerase of claim 47, wherein said modification corresponds to amino acid position K (Lys726).

59. (New) The polymerase of claim 58, wherein K (Lys726) is substituted with an amino acid selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

60. (New) The polymerase of claim 47, wherein said modifications

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correspond to amino acid at position R (Arg722) and at position K (Lys726).

61. (New) The polymerase of claim 60, wherein R (Arg722) is substituted with an amino acid selected from the group consisting of Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val, and wherein K (Lys726) is substituted with an amino acid selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

62. (New) The polymerase of claim 47, wherein said polymerase is a RNA polymerase.

63. (New) The polymerase of claim 62, wherein said RNA polymerase is selected from the group consisting of T3, T5 and SP6.

64. (New) The polymerase of claim 47, wherein said polymerase has substantially reduced or lacks 3'-5' exonuclease activity.



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